1644

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/911,423*

DATE: 03/25/98
TIME: 16:43:00

INPUT SET: S24403.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED
04-06-98

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 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: Gorman, Daniel M.
 6                       Randall, Troy D.
 7                       Zlotnik, Albert
 8
 9       (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
10              REAGENTS
11
12      (iii) NUMBER OF SEQUENCES: 8
13
14       (iv) CORRESPONDENCE ADDRESS:
15            (A) ADDRESSEE: DNAX Research Institute
16            (B) STREET: 901 California Avenue
17            (C) CITY: Palo Alto
18            (D) STATE: California
19            (E) COUNTRY: USA
20            (F) ZIP: 94304-1104
21
22        (v) COMPUTER READABLE FORM:
23            (A) MEDIUM TYPE: Floppy disk
24            (B) COMPUTER: IBM PC compatible
25            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28       (vi) CURRENT APPLICATION DATA:
29            (A) APPLICATION NUMBER: US 08/911,423
30            (B) FILING DATE: 14-AUG-1997
31            (C) CLASSIFICATION:
32
33      (vii) PRIOR APPLICATION DATA:
34            (A) APPLICATION NUMBER: US 60/023,419
35            (B) FILING DATE: 16-AUG-1996
36
37      (vii) PRIOR APPLICATION DATA:
38            (A) APPLICATION NUMBER: US 60/027,901
39            (B) FILING DATE: 07-OCT-1996
40
41     (viii) ATTORNEY/AGENT INFORMATION:
42            (A) NAME: Ching, Edwin P.
43            (B) REGISTRATION NUMBER: 34,090
44            (C) REFERENCE/DOCKET NUMBER: DX0612K
45
46       (ix) TELECOMMUNICATION INFORMATION:
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INPUT SET: S24403.raw

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47                (A) TELEPHONE: 650-852-9196
48                (B) TELEFAX: 650-496-1200
49
50
51    (2) INFORMATION FOR SEQ ID NO:1:
52
53          (i) SEQUENCE CHARACTERISTICS:
54                (A) LENGTH: 1073 base pairs
55                (B) TYPE: nucleic acid
56                (C) STRANDEDNESS: single
57                (D) TOPOLOGY: linear
58
59         (ii) MOLECULE TYPE: cDNA
60
61
62         (ix) FEATURE:
63                (A) NAME/KEY: CDS
64                (B) LOCATION: 68..751
65
66
67         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69    CTCGAGATCC ATTGTGCTGG AAAGGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG        60
70
71    AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT        109
72            Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
73             1               5                  10
74
75    GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC        157
76    Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
77     15                  20                  25                  30
78
79    CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC        205
80    Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
81                     35                  40                  45
82
83    CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT        253
84    Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
85                 50                  55                  60
86
87    GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG        301
88    Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
89                 65                  70                  75
90
91    CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT        349
92    His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
93             80                  85                  90
94
95    GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA        397
96    Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
97     95                  100                 105                 110
98
99    GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA        445
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INPUT SET: S24403.raw

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100   Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
101                   115             120             125
102

103   TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC      493
104   Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
105                   130             135             140
106

107   CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC      541
108   Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
109           145             150             155
110

111   CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC      589
112   Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
113       160             165             170
114

115   CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC      637
116   Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
117   175             180             185             190
118

119   CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC      685
120   Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
121                   195             200             205
122

123   CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT      733
124   Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
125                   210             215             220
126

127   CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC            781
128   Leu Gly Gly Arg Trp Pro
129           225
130

131   CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC    841
132

133   CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG    901
134

135   TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT    961
136

137   CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG   1021
138

139   TTTAGTAACC TGAAAAAAAA AAAAAAAGG GCGGCCGCGG AGGCCGAATT CC            1073
140

141

142   (2) INFORMATION FOR SEQ ID NO:2:
143

144           (i) SEQUENCE CHARACTERISTICS:
145                   (A) LENGTH: 228 amino acids
146                   (B) TYPE: amino acid
147                   (D) TOPOLOGY: linear
148

149           (ii) MOLECULE TYPE: protein
150

151           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
152
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INPUT SET: S24403.raw

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153   Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
154    1               5               10              15
155
156   Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
157            20               25               30
158
159   Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
160            35               40               45
161
162   Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
163            50               55               60
164
165   Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
166    65               70               75               80
167
168   Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
169            85               90               95
170
171   Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
172            100              105              110
173
174   Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
175            115              120              125
176
177   Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
178            130              135              140
179
180   Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
181    145              150              155              160
182
183   Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
184            165              170              175
185   \
186   Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
187            180              185              190
188
189   Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
190            195              200              205
191
192   Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
193    210              215              220
194
195   Gly Arg Trp Pro
196    225
197
198   (2) INFORMATION FOR SEQ ID NO:3:
199
200       (i) SEQUENCE CHARACTERISTICS:
201           (A) LENGTH: 1006 base pairs
202           (B) TYPE: nucleic acid
203           (C) STRANDEDNESS: single
204           (D) TOPOLOGY: linear
205
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INPUT SET: S24403.raw

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206        (ii) MOLECULE TYPE: cDNA
207
208
209        (ix) FEATURE:
210              (A) NAME/KEY: CDS
211              (B) LOCATION: 1..723
212
213
214        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
215
216     ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG          48
217     Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
218      1               5                  10                  15
219
220     GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC          96
221     Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
222                  20                  25                  30
223
224     GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC         144
225     Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
226                  35                  40                  45
227
228     TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG         192
229     Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
230           50                  55                  60
231
232     GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC         240
233     Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
234      65                  70                  75                  80
235
236     TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA         288
237     Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
238                  85                  90                  95
239
240     GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT         336
241     Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
242                 100                 105                 110
243
244     ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC         384
245     Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
246                 115                 120                 125
247
248     AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT         432
249     Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
250                 130                 135                 140
251
252     GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA         480
253     Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
254     145                 150                 155                 160
255
256     GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC         528
257     Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
258                 165                 170                 175
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/911,423*

INPUT SET: S24403.raw

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